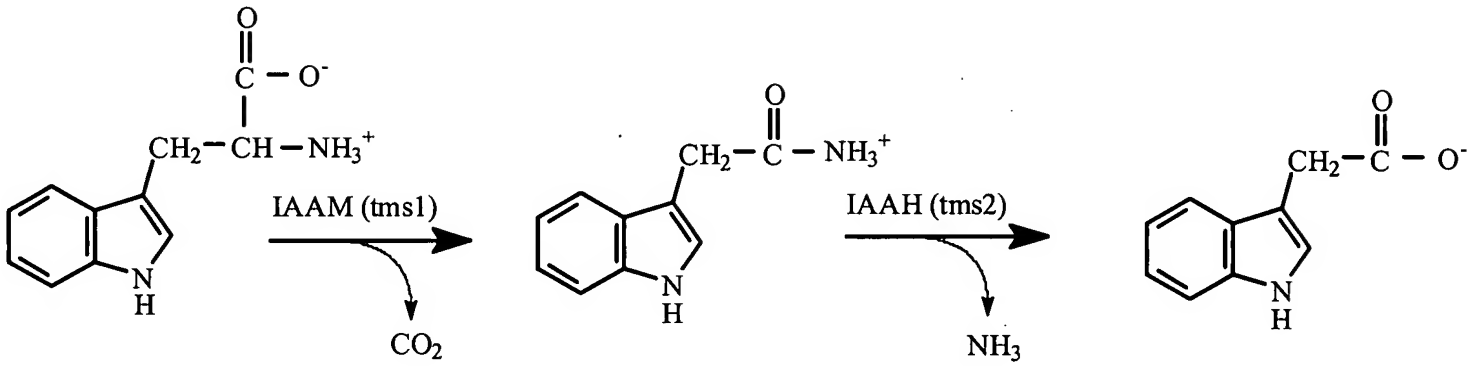


Tryptophan

Indole-3-acetamide (IAM)

Indole-3-acetic acid (IAA)
(toxic to plants)

Fig. 1

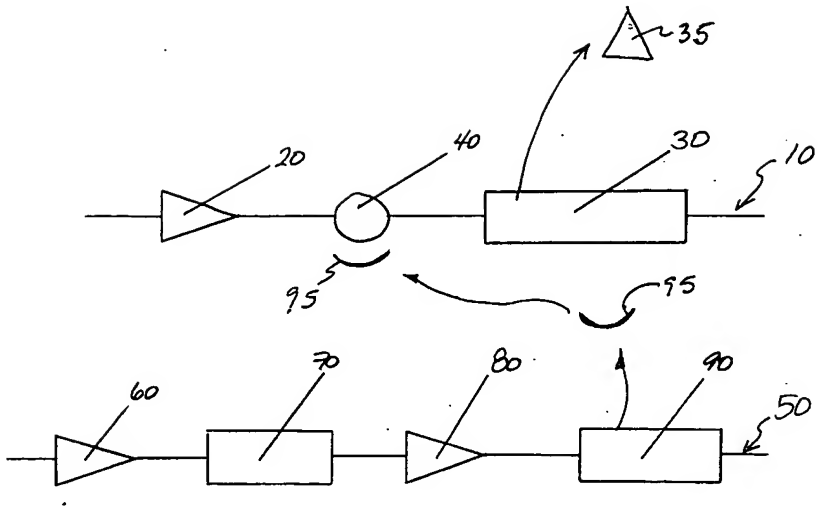


Fig. 2

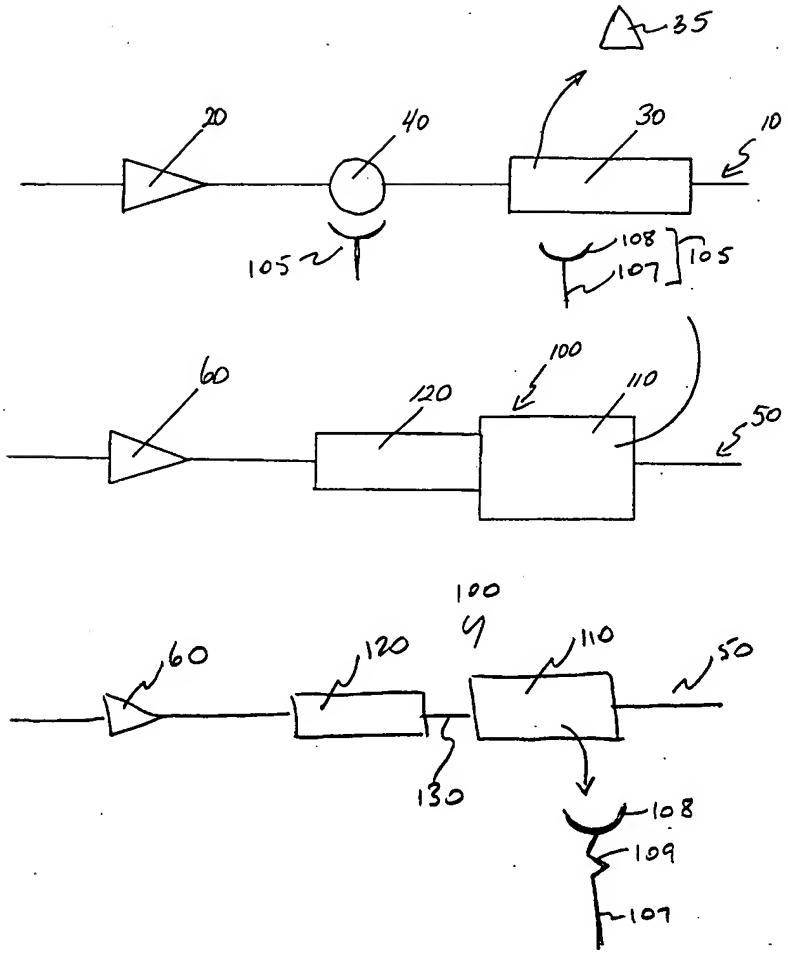

35
20
40
30
10
105
108
107
105
60
120
100
110
50
100
60
120
110
50
130
108
109
107

Fig. 3

Fig. 4A

ROS Inverted Repeat
DNA Binding Sites(Operator sequences)

TATATTTCAA-TTTTA-**TTGTAATATA** *virC/virD*
**** ** ** * *** *** **
TATAATTAAAATATTAA**CTGTCGCATT** *ipt*

Fig. 4B

Comparison of ROS DNA Binding Site (Operator) Sequences

VirC/VirD	**TATATTTCAA**
	TATATTACAA
ipt	**TATAATTAAA**
	AATGCGACAG
	TATAHTtCAA
	a g gaa g
Consensus	**WATDHWKMAR**

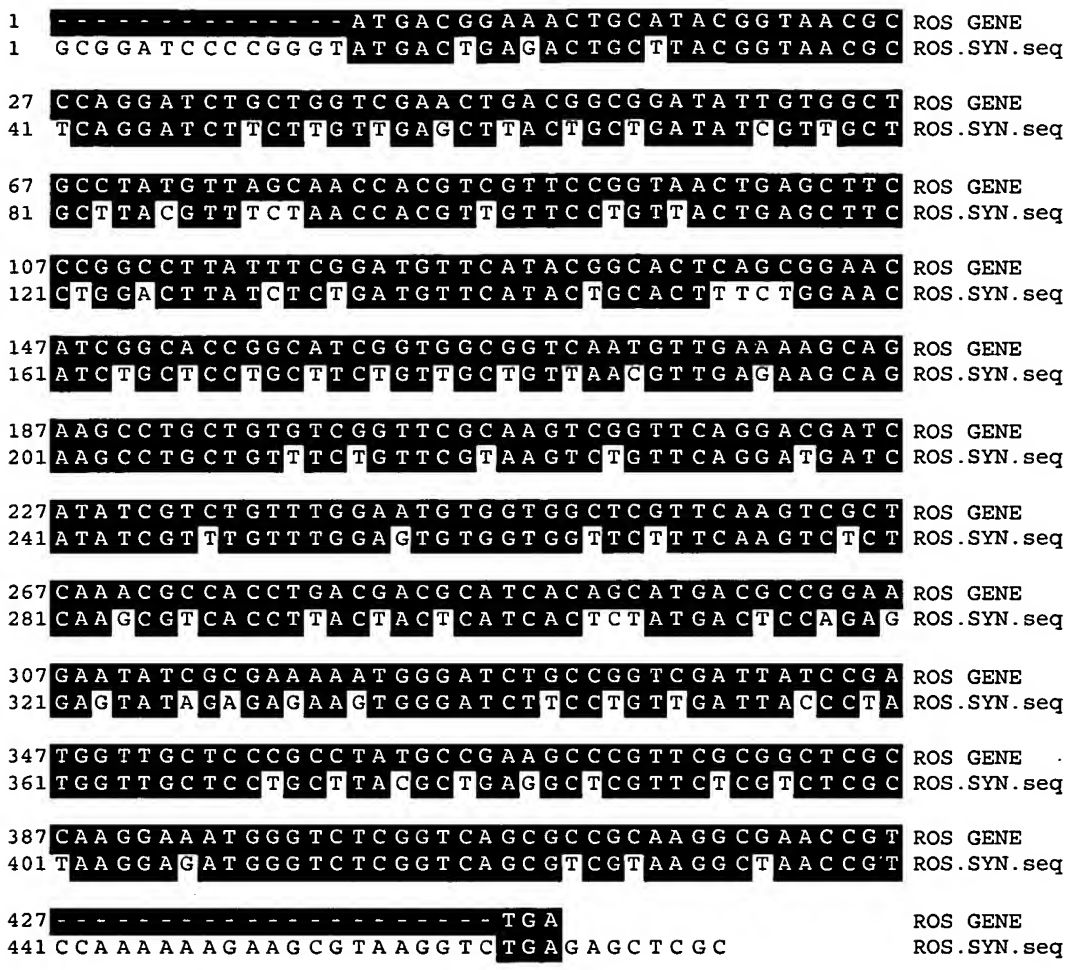

1 ---------------ATGACGGAAACTGCATACGGTAACGC ROS GENE
1 GCGGATCCCCGGGTATGACTGAGACTGCTTACGGTAACGC ROS.SYN.seq
27 CCAGGATCTGCTGGTCGAACTGACGGCGGATATTGTGGCT ROS GENE
41 TCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTGCT ROS.SYN.seq
67 GCCTATGTTAGCAACCACGTCGTTCCGGTAACTGAGCTTC ROS GENE
81 GCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTC ROS.SYN.seq
107 CCGGCCTTATTTCGGATGTTCATACGGCACTCAGCGGAAC ROS GENE
121 CTGGACTTATCTCTGATGTTCATACTGCACTTTCTGGAAC ROS.SYN.seq
147 ATCGGCACCGGCATCGGTGGCGGTCAATGTTGAAAAGCAG ROS GENE
161 ATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGCAG ROS.SYN.seq
187 AAGCCTGCTGTGTCGGTTCGCAAGTCGGTTCAGGACGATC ROS GENE
201 AAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATC ROS.SYN.seq
227 ATATCGTCTGTTTGGAATGTGGTGGCTCGTTCAAGTCGCT ROS GENE
241 ATATCGTTTGTTTGGAGTGTGGTGGTTCTTTCAAGTCTCT ROS.SYN.seq
267 CAAACGCCACCTGACGACGCATCACAGCATGACGCCGGAA ROS GENE
281 CAAGCGTCACCTTACTACTCATCACTCTATGACTCCAGAG ROS.SYN.seq
307 GAATATCGCGAAAAATGGGATCTGCCGGTCGATTATCCGA ROS GENE
321 GAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTA ROS.SYN.seq
347 TGGTTGCTCCCGCCTATGCCGAAGCCCGTTCGCGGCTCGC ROS GENE
361 TGGTTGCTCCTGCTTACGCTGAGGCTCGTTCTCGTCTCGC ROS.SYN.seq
387 CAAGGAAATGGGTCTCGGTCAGCGCCGCAAGGCGAACCGT ROS GENE
401 TAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCTAACCGT ROS.SYN.seq
427 ----------TGA ROS GENE
441 CCAAAAAAGAAGCGTAAGGTCTGAGAGCTCGC ROS.SYN.seq

Fig. 4C

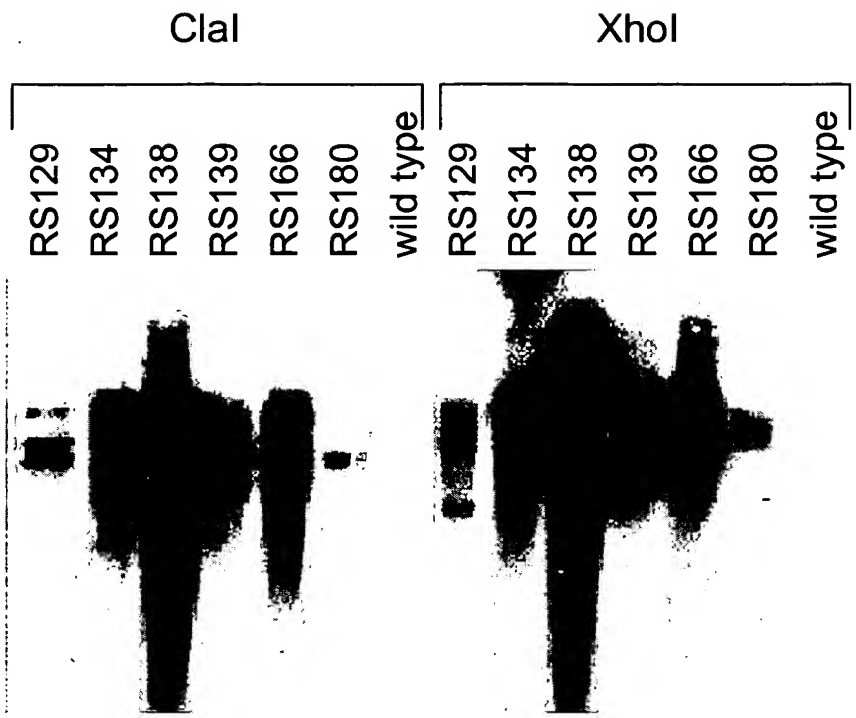

ClaI
XhoI
RS129
RS134
RS138
RS139
RS166
RS180
wild type
RS129
RS134
RS138
RS139
RS166
RS180
wild type

Fig. 4D

p74-101

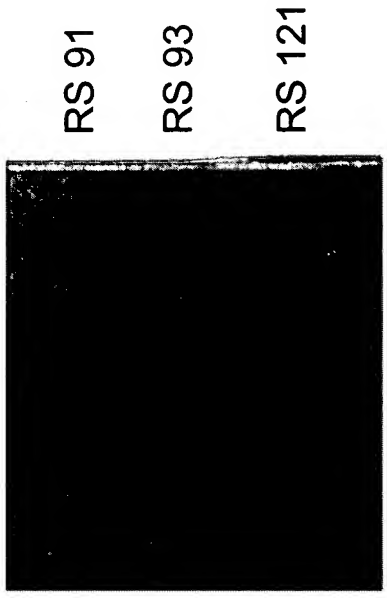


Fig. 4E

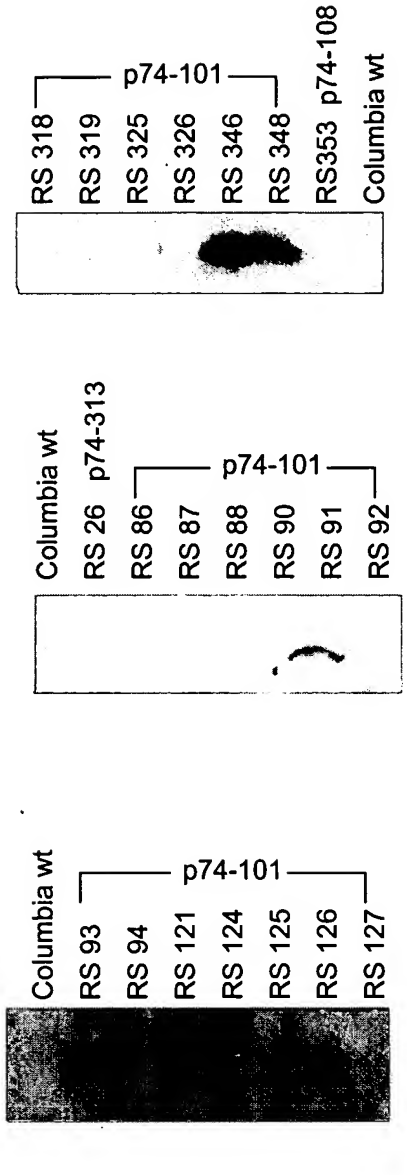

RS 318
RS 319
p74-101
RS 325
RS 326
RS 346
RS 348
RS353
p74-108
Columbia wt
Columbia wt
RS 26
p74-313
RS 86
RS 87
p74-101
RS 88
RS 90
RS 91
RS 92
Columbia wt
RS 93
RS 94
p74-101
RS 121
RS 124
RS 125
RS 126
RS 127

Fig. 4F

Columbia wt

pB1121

p74-501

buffer

Fig. 4G

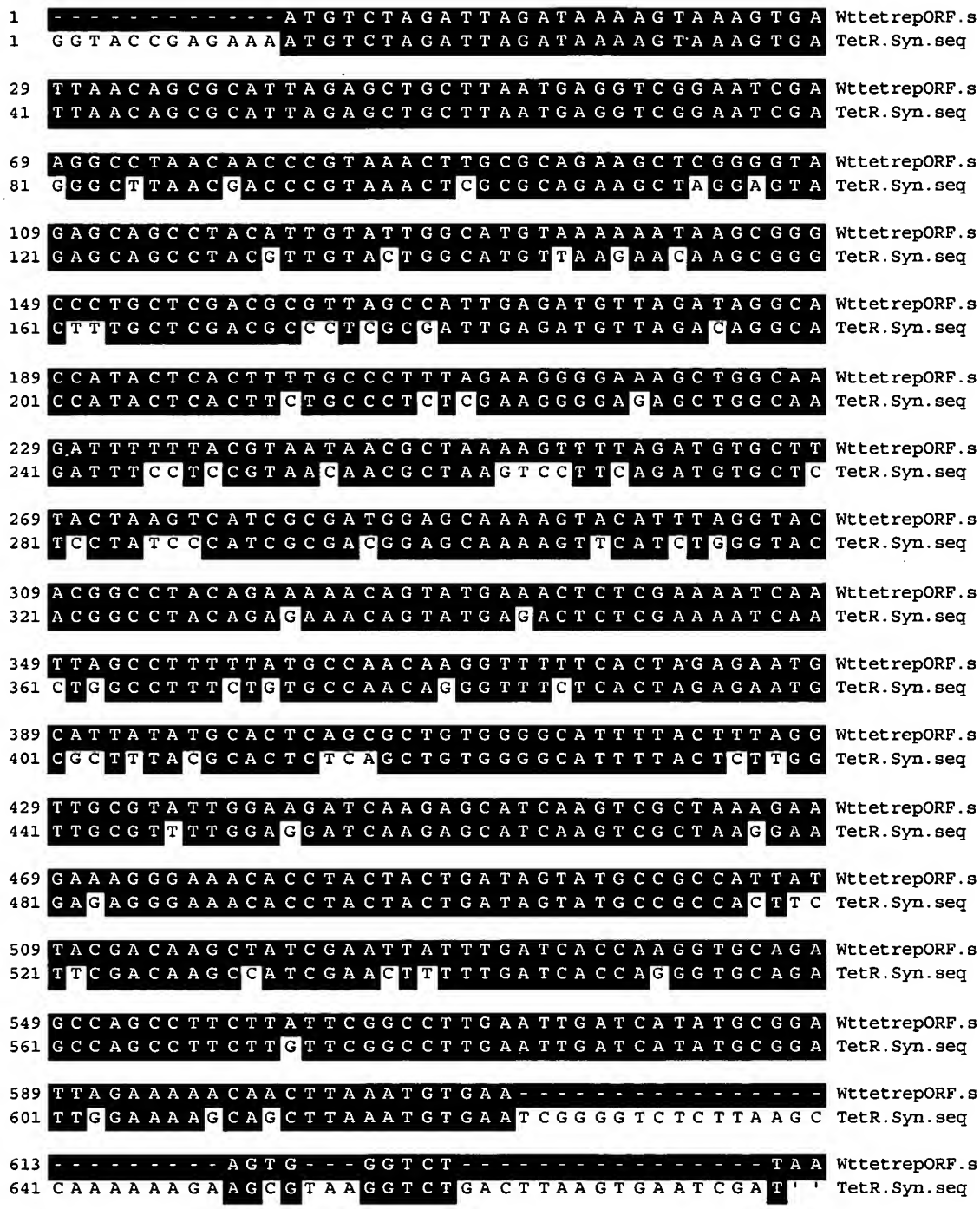

1 ---------- ATGTCTAGATTAGATAAAAGTAAAGTGA WttetrepORF.s
1 GGTACCGAGAAA ATGTCTAGATTAGATAAAAGTAAAGTGA TetR.Syn.seq
29 TTAACAGCGCATTAGAGCTGCTTAATGAGGTCGGAATCGA WttetrepORF.s
41 TTAACAGCGCATTAGAGCTGCTTAATGAGGTCGGAATCGA TetR.Syn.seq
69 AGGCCTAACAACCCGTAAACTTGCGCAGAAGCTCGGGGTA WttetrepORF.s
81 GGGCTTAACGACCCGTAAACTCGCGCAGAAGCTAGGAGTA TetR.Syn.seq
109 GAGCAGCCTACATTGTATTGGCATGTAAAAAATAAGCGGG WttetrepORF.s
121 GAGCAGCCTACGTTGTACTGGCATGTTAAGAACAAGCGGG TetR.Syn.seq
149 CCCTGCTCGACGCGTTAGCCATTGAGATGTTAGATAGGCA WttetrepORF.s
161 CTTTGCTCGACGCCCTCGCGATTGAGATGTTAGACAGGCA TetR.Syn.seq
189 CCATACTCACTTTTGCCCTTTAGAAGGGGAAAGCTGGCAA WttetrepORF.s
201 CCATACTCACTTCTGCCCTCTCGAAGGGGAGAGCTGGCAA TetR.Syn.seq
229 GATTTTTTACGTAATAACGCTAAAAGTTTTAGATGTGCTT WttetrepORF.s
241 GATTTCCTCCGTAACAACGCTAAGTCCTTCAGATGTGCTC TetR.Syn.seq
269 TACTAAGTCATCGCGATGGAGCAAAAGTACATTTAGGTAC WttetrepORF.s
281 TCCTATCCCATCGCGACGGAGCAAAAGTTCATCTGGGTAC TetR.Syn.seq
309 ACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAATCAA WttetrepORF.s
321 ACGGCCTACAGAGAAACAGTATGAGACTCTCGAAAATCAA TetR.Syn.seq
349 TTAGCCTTTTTTATGCCAACAAGGTTTTTCACTAGAGAATG WttetrepORF.s
361 CTGGCCTTTCTGTGCCAACAGGGTTTCTCACTAGAGAATG TetR.Syn.seq
389 CATTATATGCACTCAGCGCTGTGGGGCATTTTACTTTAGG WttetrepORF.s
401 CGCTTTACGCACTCTCAGCTGTGGGGCATTTTACTCTTGG TetR.Syn.seq
429 TTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAA WttetrepORF.s
441 TTGCGTTTTGGAGGATCAAGAGCATCAAGTCGCTAAGGAA TetR.Syn.seq
469 GAAAGGGAAACACCTACTACTGATAGTATGCCGCCATTAT WttetrepORF.s
481 GAGAGGGAAACACCTACTACTGATAGTATGCCGCCACTTC TetR.Syn.seq
509 TACGACAAGCTATCGAATTATTTGATCACCAAGGTGCAGA WttetrepORF.s
521 TTCGACAAGCCATCGAACTTTTTGATCACCAGGGTGCAGA TetR.Syn.seq
549 GCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGA WttetrepORF.s
561 GCCAGCCTTCTTGTTCGGCCTTGAATTGATCATATGCGGA TetR.Syn.seq
589 TTAGAAAAACAACTTAAATGTGAA---------- WttetrepORF.s
601 TTGGAAAAGCAGCTTAAATGTGAATCGGGGTCTCTTAAGC TetR.Syn.seq
613 ---------- AGTG---GGTCT---------- TAA WttetrepORF.s
641 CAAAAAAGAAGCGTAAGGTCTGACTTAAGTGAATCGAT' ' TetR.Syn.seq

Fig. 5

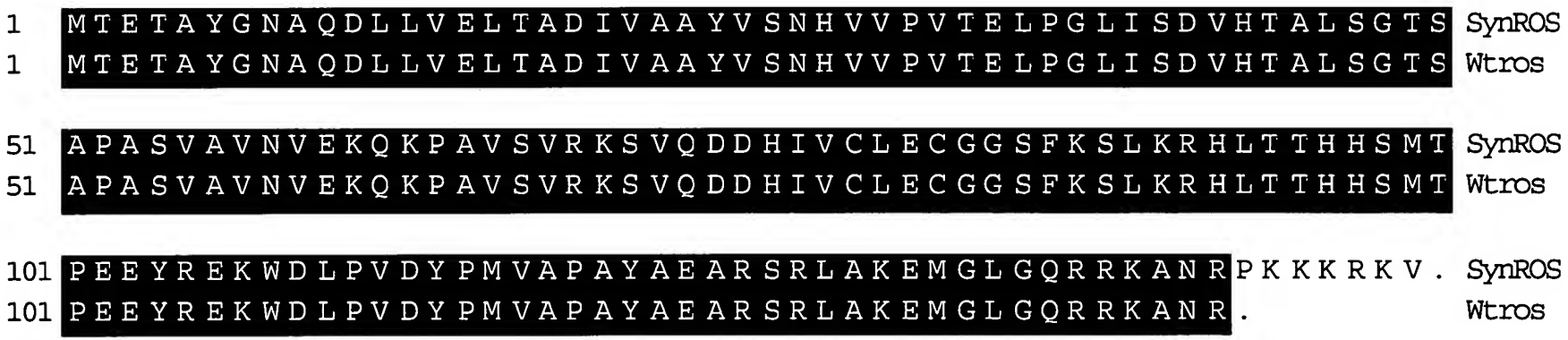

1 MTETAYGNAQDLLVELTADIVAAYVSNHVVPVTELPGLISDVHTALSGTS SynROS
1 MTETAYGNAQDLLVELTADIVAAYVSNHVVPVTELPGLISDVHTALSGTS Wtros
51 APASVAVNVEKQKPAVSVRKSVQDDHIVCLECGGSFKSLKRHLTTHHSMT SynROS
51 APASVAVNVEKQKPAVSVRKSVQDDHIVCLECGGSFKSLKRHLTTHHSMT Wtros
101 PEEYREKWDLPVDYPMVAPAYAEARSRLAKEMGLGQRRKANRPKKKRKV. SynROS
101 PEEYREKWDLPVDYPMVAPAYAEARSRLAKEMGLGQRRKANR. Wtros

Fig. 6

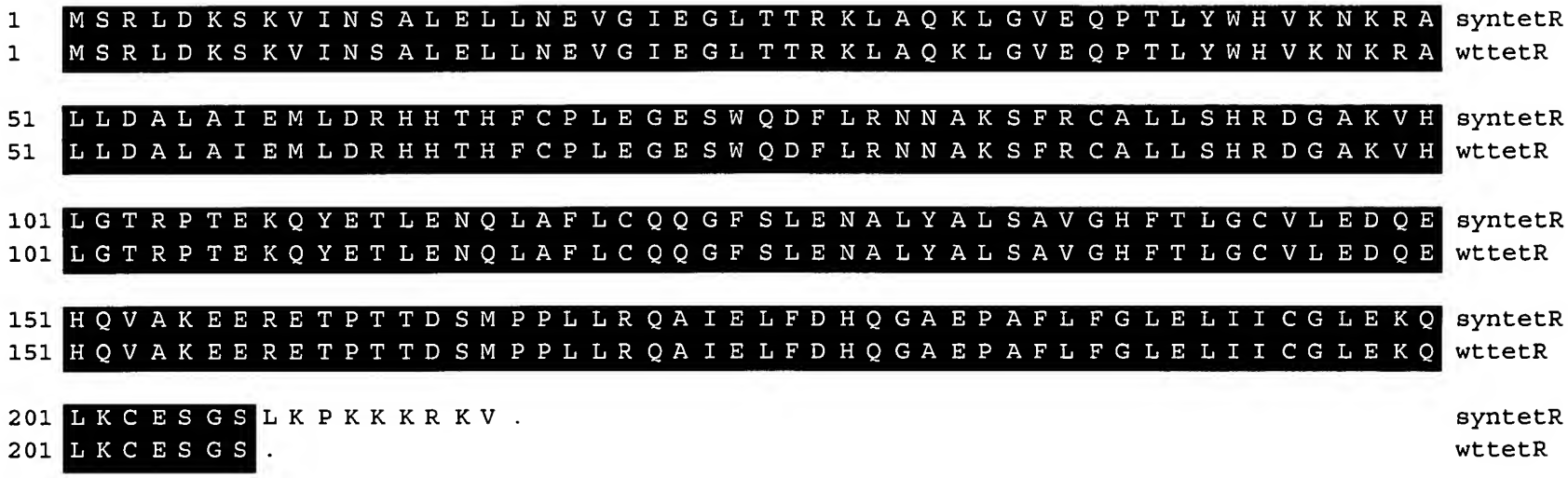

1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRA syntetR
1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRA wttetR
51 LLDALAIEMLDRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVH syntetR
51 LLDALAIEMLDRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVH wttetR
101 LGTRPTEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQE syntetR
101 LGTRPTEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQE wttetR
151 HQVAKEERETPTTDSMPPLLRQAIELFDHQGAEPAFLFGLELIICGLEKQ syntetR
151 HQVAKEERETPTTDSMPPLLRQAIELFDHQGAEPAFLFGLELIICGLEKQ wttetR
201 LKCESGSLKPKKKRKV. syntetR
201 LKCESGS. wttetR

Fig. 7

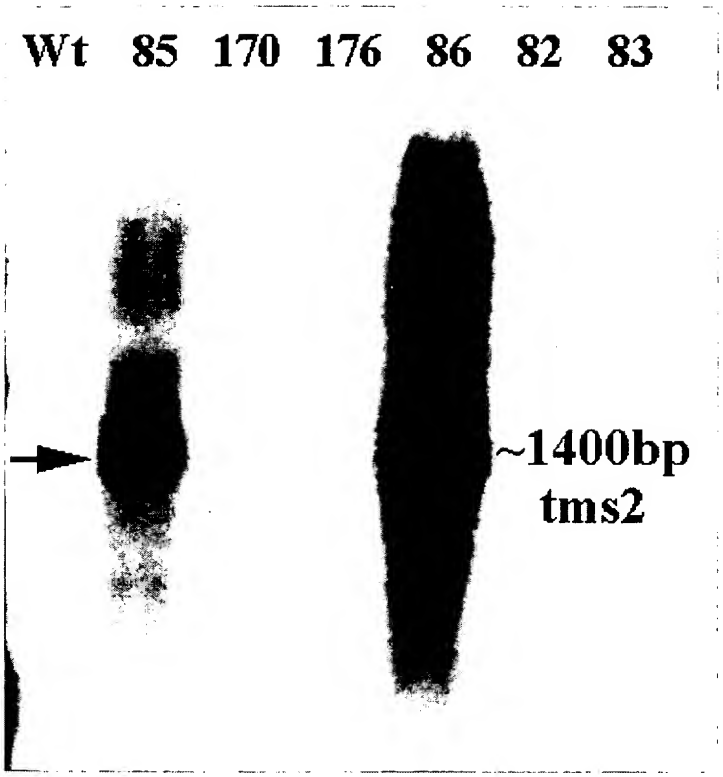


Fig. 8

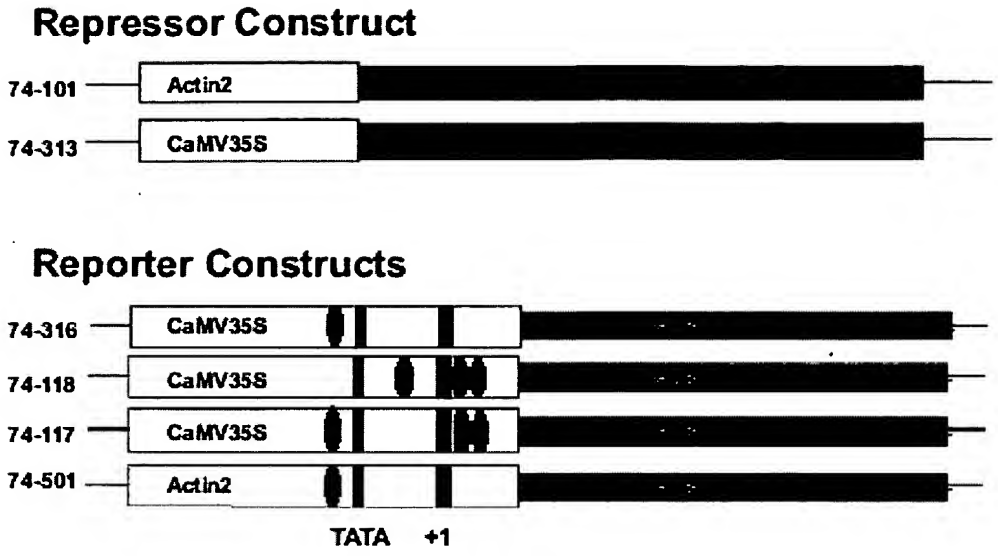
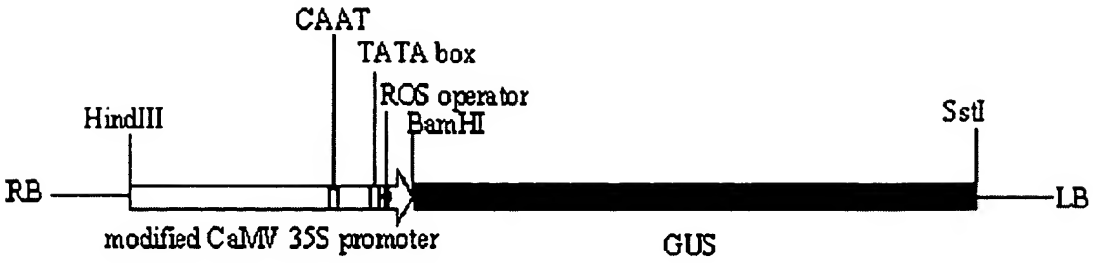
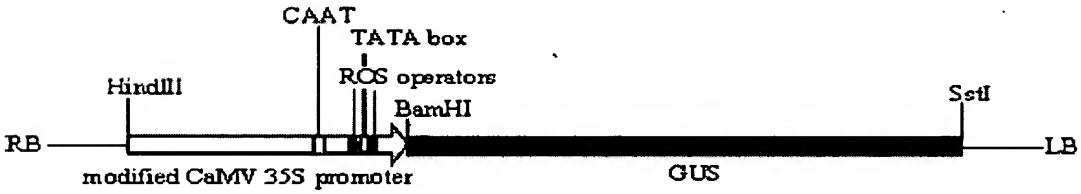

Repressor Construct
74-101
Actin2
74-313
CaMV35S
Reporter Constructs
74-316
CaMV35S
74-118
CaMV35S
74-117
CaMV35S
74-501
Actin2
TATA
+1

Fig. 9A



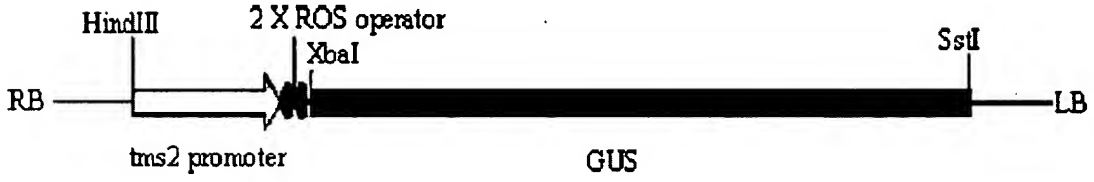
p74-315

Fig. 9B



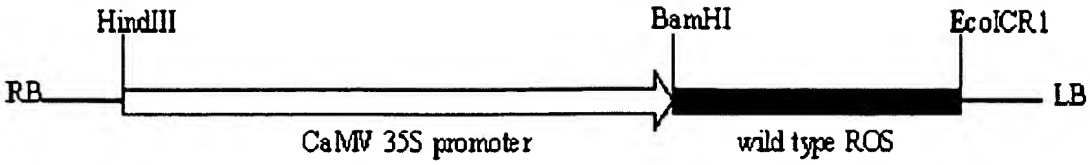
p74-309

Fig. 9C



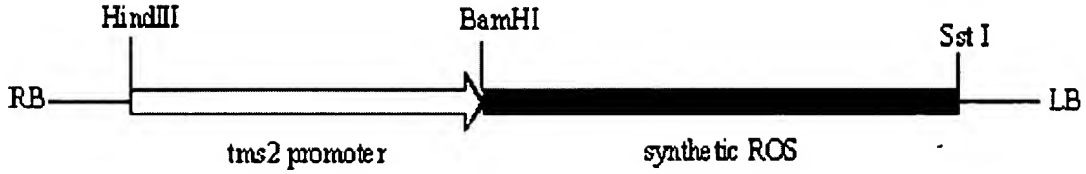
p76-508

Fig. 9D



p74-107

Fig. 9E



p74-108

Fig. 9F

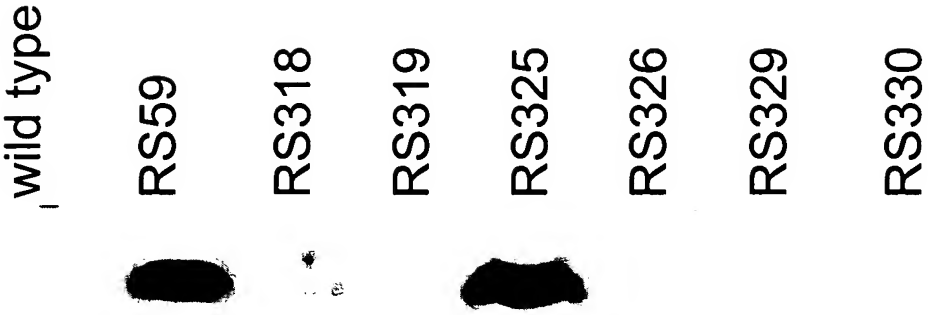


Fig. 10A

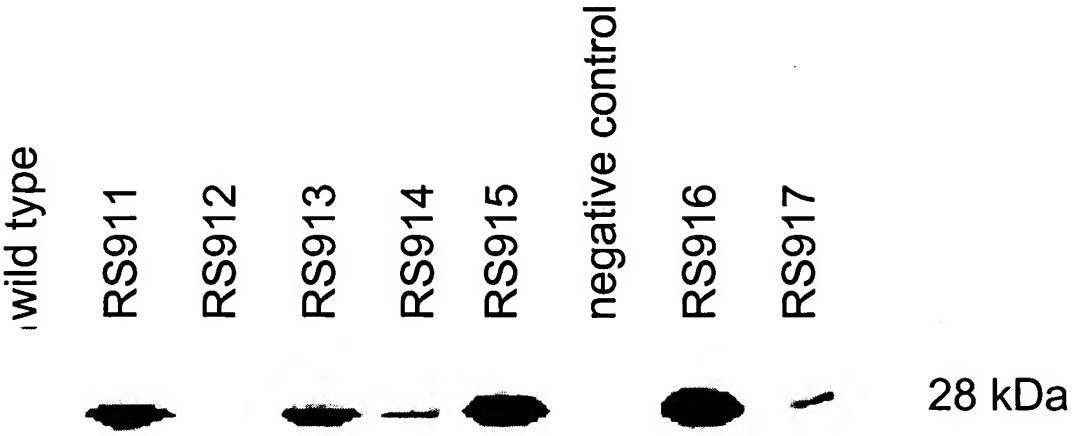


Fig. 10B

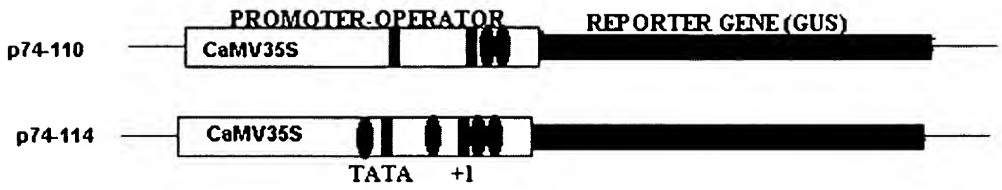

PROMOTER-OPERATOR
REPORTER GENE (GUS)
p74-110
CaMV35S
p74-114
CaMV35S
TATA
+1

Fig. 11

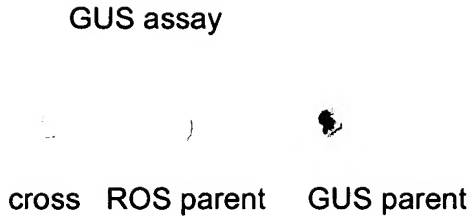


Fig. 12A

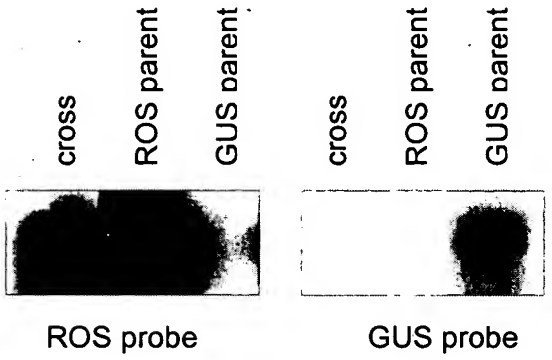


Fig. 12B

GUS probe ROS probe

Southern blot

Fig. 12C

Fig. 13A

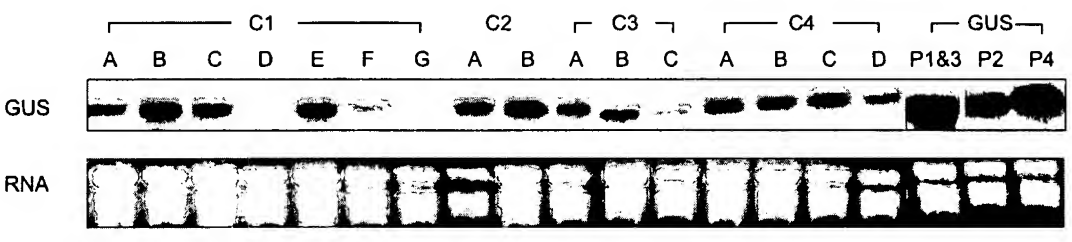


Fig. 13B

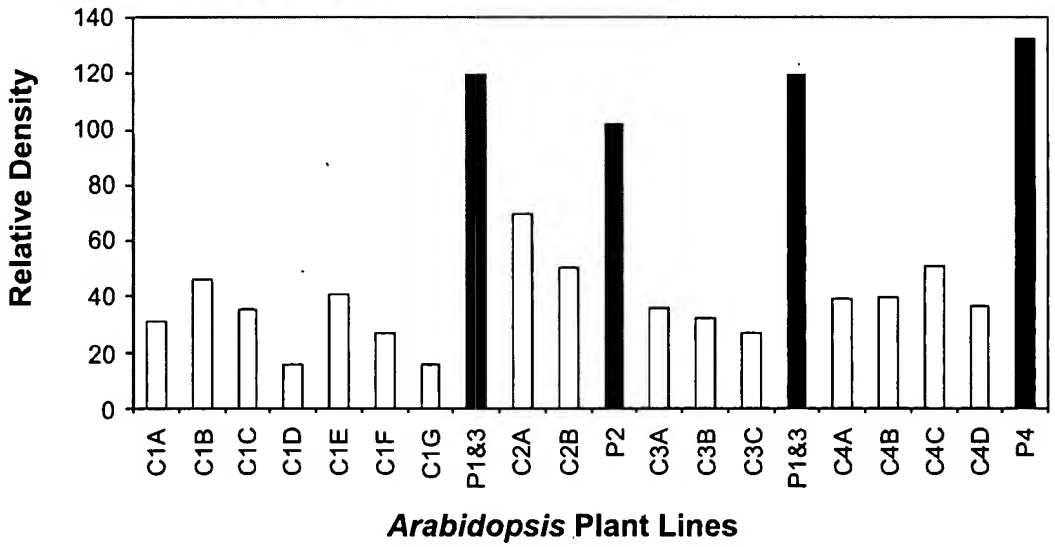


Fig. 13

Fig. 14A

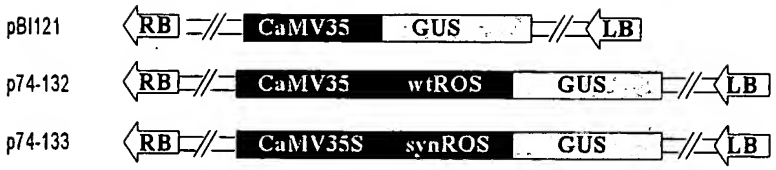
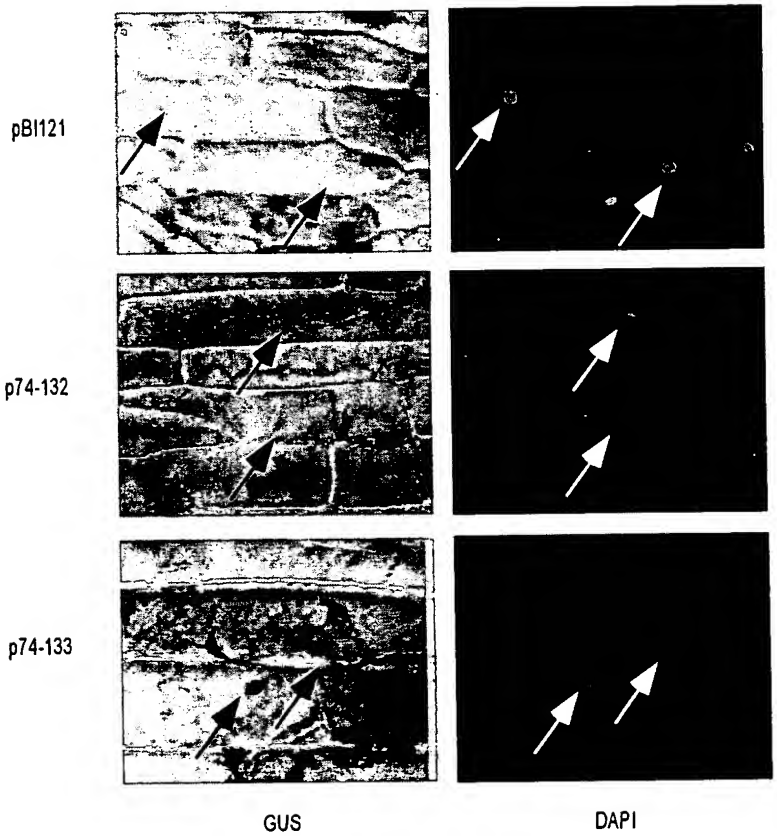


Fig. 14B



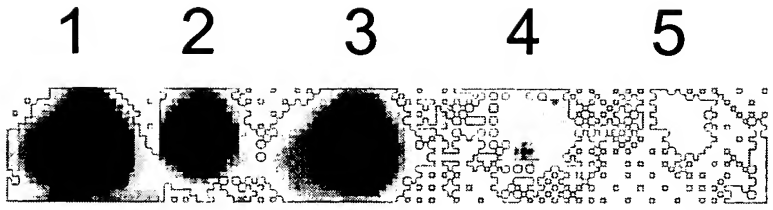


Fig. 15

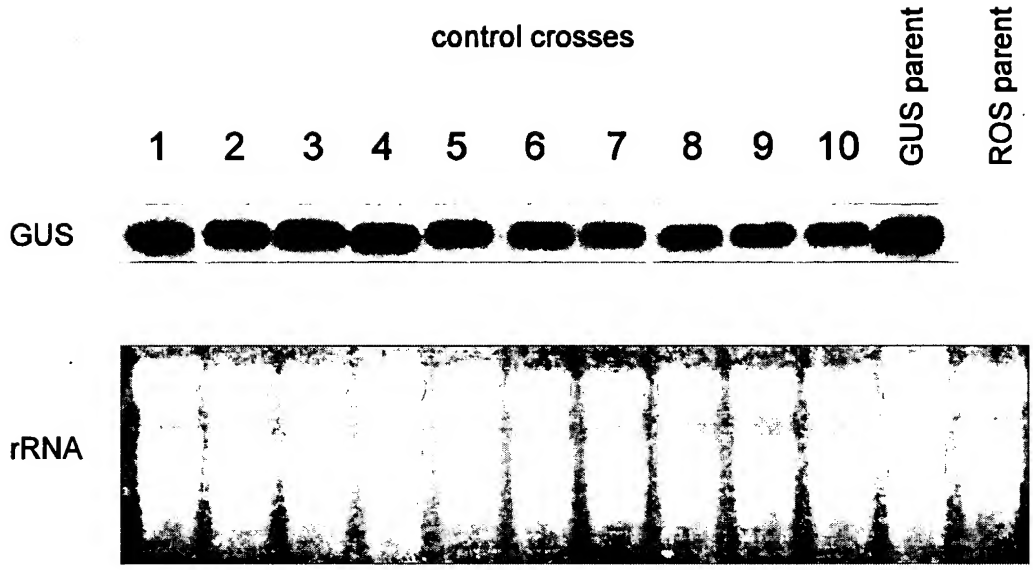


Fig. 16A

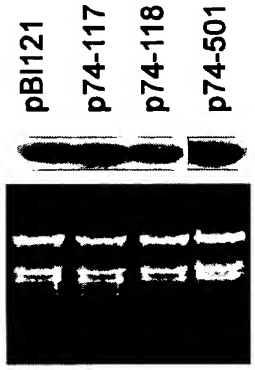


Fig. 16B

Fig. 17A

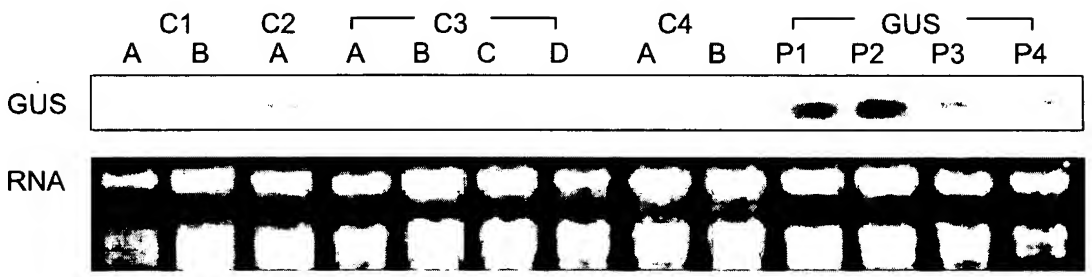


Fig. 17B

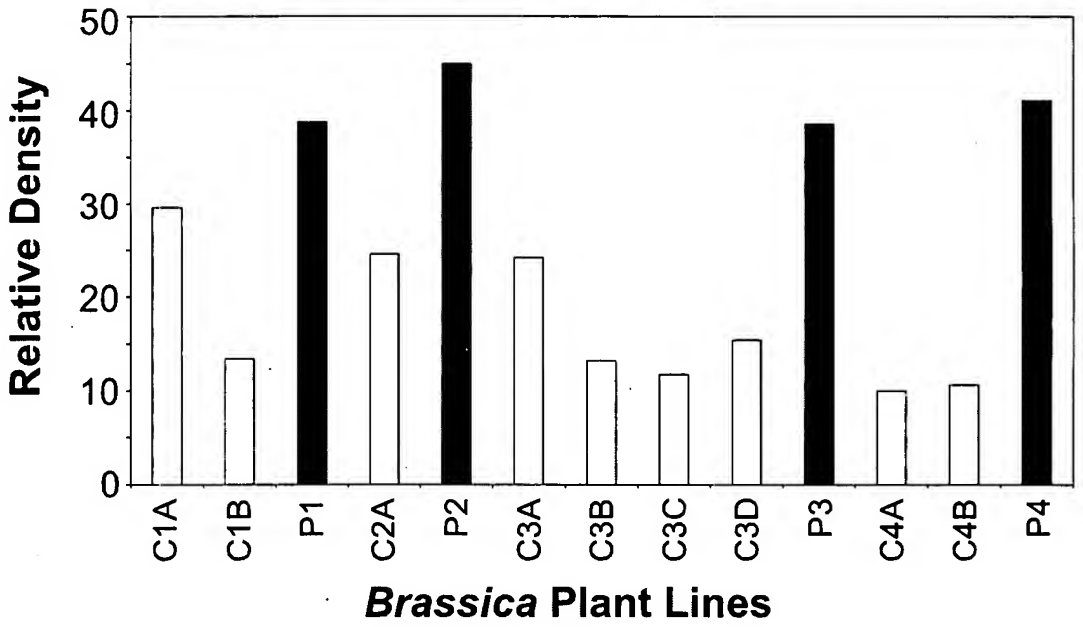


Fig. 17